

SEQUENCE LISTING

SEQ ID NO:1

SEQUENCE LENGTH: 4276

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

CELL TYPE: leukocyte

SEQUENCE DESCRIPTION: SEQ ID NO:1

TTCTACCGTT	TTTCCCTGC	TTTCTATTCC	AGGTCACTCT	TCACTGTTTC	CG	ATG	GAA	58								
						Met	Glu									
						1										
GAT	GGA	TTC	TTG	CAT	GAT	GCC	CGT	GGG	GAT	CAG	CCT	CTT	CAT	AGT	GGC	106
Asp	Gly	Phe	Leu	Asp	Asp	Gly	Arg	Gly	Asp	Gln	Pro	Leu	His	Ser	Gly	
						5	10	15								
CTG	GCT	TCA	CCT	CAC	TCC	TTC	ACT	CAC	CAG	AAT	GGG	GAG	AGA	CTG	GAA	154
Leu	Gly	Ser	Pro	His	Cys	Phe	Ser	His	Gln	Asn	Gly	Glu	Arg	Val	Glu	
						20	25	30								
CGA	TAT	TCT	CGA	AAC	GTG	TTT	GTA	GGC	GGG	TTG	CCT	CCA	GAC	ATT	CAT	202
Arg	Tyr	Ser	Arg	Lys	Val	Phe	Val	Gly	Gly	Gly	Leu	Pro	Pro	Asp	Ile	Asp
						35	40	45								
GAA	GAT	GAC	ATC	ACA	GCT	ACT	TTT	CGT	CCC	TTT	GGC	CCT	CTG	ATT	GTG	250
Glu	Asp	Glu	Ile	Thr	Ala	Ser	Phe	Arg	Arg	Phe	Gly	Pro	Leu	Ile	Val	
						55	60	65								
GAT	TGG	CCT	CAT	AAA	GCT	GAG	AGC	AAA	TCC	TAT	TTT	CCT	CCT	AAA	GGC	298
Asp	Trp	Pro	His	Lys	Ala	Glu	Ser	Lys	Ser	Tyr	Phe	Pro	Pro	Lys	Gly	
						70	75	80								
TAT	GCA	TTC	CTG	CTG	TTT	CAA	GAT	GAA	AGC	TCT	GTG	CAG	GCT	CTC	ATT	346
Tyr	Ala	Phe	Leu	Leu	Phe	Gln	Asp	Glu	Ser	Ser	Val	Gln	Ala	Leu	Ile	
						85	90	95								
GAT	GCA	TCC	ATT	CAA	CAA	GAT	GGA	AAA	CTC	TAC	CTT	TGT	GTA	TCA	ACT	394
Asp	Ala	Cys	Ile	Glu	Glu	Asp	Gly	Lys	Leu	Tyr	Leu	Cys	Val	Ser	Ser	
						100	105	110								
CCC	ACT	ATC	AAC	CAT	AAG	CCA	GTC	CAG	ATT	CCG	CCT	TGG	AAT	CTC	ACT	442
Pro	Thr	Ile	Lys	Asp	Lys	Pro	Val	Gln	Ile	Arg	Pro	Trp	Asn	Leu	Ser	
						115	120	125								
GAC	AGT	GAC	TTT	GTG	ATG	GAT	GGT	TCA	CAG	CCA	CTT	GAC	CCA	CGA	AAA	490
Asp	Ser	Asp	Phe	Val	Met	Asp	Gly	Ser	Gln	Pro	Leu	Asp	Pro	Arg	Lys	
						135	140	145								
ACT	ATA	TTT	GTT	GGT	GGT	CCT	CGA	CCA	TTA	CGA	GCT	GTG	GAG	CTT		538
Thr	Ile	Phe	Val	Gly	Gly	Val	Pro	Arg	Pro	Leu	Arg	Ala	Val	Glu	Leu	

	150	155	160	
GCG ATG GTA ATG GAT CGG CTA TAC GGA GGT GTG TGC TAC GCT GGG ATT				586
Ala Met Val Met Asp Arg Leu Tyr Gly Gly Val Cys Tyr Ala Gly Ile				
165	170	175		
GAT ACC GAC CCT GAG CTA AAA TAC CCA AAA GGA GCT GGG AGA GTT GCG				634
Asp Thr Asp Pro Glu Leu Lys Tyr Pro Lys Gly Ala Gly Arg Val Ala				
180	185	190		
TTC TCT AAT CAA CAG AGT TAC ATA GCT GCT ATC AGT GCC CGC TTT GTT				682
Phe Ser Asn Gln Gln Ser Tyr Ile Ala Ala Ile Ser Ala Arg Phe Val				
195	200	205	210	
CAG CTG CAG CAT GGA GAG ATA GAT AAA CCG GTA AGC CTT ATA CTA CAT				730
Gln Leu Gln His Gly Glu Ile Asp Lys Arg Val Ser Leu Ile Leu His				
215	220	225		
TTT GGA AAA TTC TAGAAATGGT CCTCTAAATG TGTGATTACC AATATTAGAA				782
Phe Gly Lys Phe				
230				
CGGGAGCATT TTATGACAAT AAAGTGACAG CTGACAATTG TGCCATAGA GTTAATTATG				842
GTCTATAATA CATGAAATAA TGTCCTATGA ATTTCCTTTA TCTTCAGTT TTTTGGTAG				902
CCTAACATCGA ACACATACAAT TTACTTGAGT TAATTAAATC TTCTCTAACT TCCATTCAAT				962
CTCAATCCAT CCGTCCATTG ATTCACTTAG TTGTGAAGTC ATTCAATAAA TATTTACTGA				1022
ATCCTTGTGTT CTGTGTTATA TCAAGTATAC AAACAGGAAT GCCCTTGAGG TTTCTGCCCC				1082
TTTTTTTGTGTTTGTGTTATA ATCCTGGAC ATAGGGAAGA CCTCAGCAAG CCCTATTCT				1142
CAATGAATTG TACTCACAGA TTTCCTTTT TTTTTTTT TCTTTTCCA CAGCCGCCAC				1202
CTCTCACCGA TTTCCTTCTT AGCTTGGTGT TTCACTGTATT CAACAAACGT TTTAGTGCTT				1262
AGGGCAAGAA GTTCTCTCC TCATGAGTTT ATTTCTTAGC AGATAGAACT GTATCACTTG				1322
CCAGTACTAC TCAGAGTGTG CCCTGTGGAC TCACTCCAG TCTGTAAACT TAGTTGTAG				1382
TGAGATAGGA ATTAGACCA GAATGTGAA TCAACCACAT TACTGGGCAC AATGTTTGGT				1442
CCAGCTGGCG ATTTCCTTTT CATAGAAAGC CTTTATTGAT GAGGAAGCA ATATATTGAT				1502
TTATATTTCG GGGTCACCTT TTTCATTCTAT GGCACACTGG CACTTTCTATG CATCTGACT				1562
TTGATATCCA TCACCTTGAG GCATTGTGCT AAAATAGATT GATTTATCG TGTGTTCTC				1622
AATTCAAGAT GTAAAAATCA TCAAGTCAGT AGCAGTTTTT GCTTTTTATG TTTCATGTCA				1682
TGTCAGCTCT ACTTCACTGG CAGTAAAAAA ATTAAAGATA GTGGTGGTCA TCCTACAAAC				1742
TGTGAATCTA TTAAAGAGAA AAGTATCTGT TCTATCTAA GCATGGGGGA GGGACAAGAT				1802
TAGTATGTTA ACATGCCATC TTGTTGTGTT TGAGATGGAG TCTCTCTCCG TCACCCAGGC				1862
TGGACTGCG AGTGTACAGTC TCACTCTACT CCAACCTCTG CCTCCCGGGT TCAAGTGATT				1922
CTCTCGCTT AGCCTCCCGA GTAGGTGGAA TTACAGGCAT ATACCACTAT GCCCAACAAA				1982
TGTTTGTATT TTAGTGGAG ACAGGGTTTC ACCGTGTTGG TCAGGCCAGT TTCAAACCTCC				2042
TGACCTCAAG GGATCCACCT GCCTCACCCC CTCAAGTGC TGGGATTACA GGCATGAGCC				2102
ACCCACCATG CCTGGCCCTAC TTGTTTTTTT ATGCACACTA AAAATACCT ACATCTACT				2162
GCCTTATTCC AACATAAGTT TCAGAGCTGT GGGATTGGTC ATTAGAAATT CAGACTGAAT				2222
TTGTGTTCTT CTGCAATGAA ATCCTTGCC CAGTGTTCAT GTCACTCTGT AGACATTATG				2282
GAGCAGCCATA GAGGCCAGAA GCCCAGTGC CTCCCTATGC CTGCTTCTCC TGGCTTCTGT				2342
GACACTCTTC TTCTCCCTT GTACTTTAT TTTTTAGTT AAAAATTTT TTTTAGAGGG				2402
AGGGTCTCAC TCTGTACCC AGGCTGGAGC ACAGAATCAC AATCATGACT CACTGCATGT				2462

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TCTTCTCCTT	TTGTTICATGG	CTAATCTTGG	TCAGGATTCC	TTGTCAAGAGC	TGGGTGGCAC	2522
CACTGCTGGT	GACAGCCTGC	TGTAAGGGAG	TTTCAGCCAT	GAATCTCTCC	AGACTAAAAA	2582
TAACCAGCTC	TTTCTTAGCT	GATGAATTAA	TAACCAAGTG	ACTGTTAATG	CTTGAAGGT	2642
TCACATGACA	GGTTGCCGA	TAGAACGCTG	GAACAGGCC	AGTTTTAGAA	ATTCACCTCT	2702
GACTTTAGA	CTCAGGTGAA	CCATTCTTAC	TGAGAAAGAA	CAAAGCAGGG	TTTTAGACTG	2762
TGAATCCTAT	GGCTGCATCT	TTTTTTTTT	TTAACACAGAG	TTCCAGGTGTT	GTGATTATAA	2822
CCCCAACATGT	GTACACTATA	AATAGAAACC	ACGAGCCAGG	CTTTTACCA	CACCTCAGAA	2882
TCTTGTGACG	CGTAGTCAG	GCATCTTCAC	ACCGACTTGA	ATATTGAAGT	GCAGTTGTG	2942
GGAACTTGGG	TCATCTTAGT	TGATTTGTT	AAAATTATGA	TTCCACATAT	GACAAAAATC	3002
CAGATCCACT	AATTAAATG	AGGGTTTATG	TCTATGAATA	ATCTCTGTG	GGTTTAATCT	3062
CATAACATTC	TAGTCTAAC	AGTIGCTTC	ACTTCATGAT	GTCTGCTCAA	ATCTTTTTC	3122
CTTTAAAGGA	TGTTTTTTA	ATAAGAAAAA	AAATGTTAAA	TGATAGATAA	AAAAGCCTT	3182
ACTAGGTCT	AAAAGATGA	ACTATCCATA	TTTCACTAAA	TGAATAATT	GTCTTCTTC	3242
TTTGGGCACC	TTGGAACAGA	TTICATTCAGA	TAGTGGGTGG	AAATGTACAT	GTATGGTAAG	3302
CATTGCTGCC	CTAGTCACTG	AAAAATGTA	ACTTCATTTT	TGATTTGCG	GTGGAAGTTA	3362
AGCCATATGT	CTTGGATGAT	CAGCTGTG	ATGAATGTC	GGGGGCCGT	TGTGGGGGGA	3422
AATTGCTCC	ATTTTCTGT	GCTAATGTTA	CCTGTCGCA	GTATTACTGT	GAATATTGCT	3482
GGGCTGCTAT	CCATTCTCGT	GCTGGCAGGG	AATCCACAA	GCCCCTGGT	AAGGAAGGCG	3542
GTGACCCGCC	TGGCATATT	TCATTCCGT	GGAACTAAAG	GATACTGCA	GTGCTCATTT	3602
TCAGGCCTCA	GAATAAGTGC	ACTCTCTGT	TCATTCTGAC	CCCTTCTCA	ACCTCTTCAC	3662
GCTGGCATGT	CTTTTGTAG	CAGTCGTAA	CTTAACATATA	GTATAATGAA	AAGAATGACC	3722
TATAATATAG	GTGTTTGTA	GATTCTGTG	TCACTGAAA	CAATATGAC	TCCCTTTTCG	3782
TATTGCCATC	GGGTTCATG	GAAGTTTAT	TCTCTGTTT	TGCTGAAAC	CAAGAGGATC	3842
CAAACCTCT	GCAACATTT	CTTAAGGGAG	AGAGAGAAAT	ATTAAGAG	AAATGAAACA	3902
ATAGAGTATT	TGGGTTTTT	AAATTAAATA	TGTTAATAA	TATAACATAT	AAGAATACTT	3962
TTATTAAAT	AACCATGCA	CAATAACACT	ATCGGTCTAT	CTGACAGTT	TTCCCCCAGG	4022
GAAGTGTCTT	TGCCCTTICC	TTTCTTTTT	TTTTTTTTC	ATCTTTTTG	TTCTCTCTCT	4082
TTTTTCCATC	CTTTTTAAT	TTTTTAACA	GCAATGGAGG	AAGTTAACAA	TTTTAATGG	4142
AAAGAGCATG	TTAGACAAA	CAAATGCATA	AGCAAGACTG	AGCAGCATT	TAATTAATT	4202
TCAGGGTTT	GAGGCTGAAC	ATAATTCT	TATCCCTAA	AAAGTTACCA	CCACATCAGA	4262
AAAAAAAAAA	AAAA					4276

SEQ ID NO:2

SEQUENCE LENGTH: 2689

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

CELL TYPE: leukocyte

SEQUENCE DESCRIPTION: SEQ ID NO:2

GTGGAGGTT	CTGGGGCGCA	GAACCGCTAC	TGCTGCTTCG	GTCTCTCCTT	GGGAAAAAAT	60
AAAATTGAA	CCTTTGGAG	CTGTGTGCTA	AATCTTCAGT	GGGACA	ATG GGT TCA	115

Met Gly Ser	
1	
GAC AAA AGA CTG ACT AGA ACA GAG CGT ACT GGA AGA TAC GGT TCC ATC	163
Asp Lys Arg Val Ser Arg Thr Glu Arg Ser Gly Arg Tyr Gly Ser Ile	
5 10 15	
ATA GAC AGG GAT GAC CGT GAT GAG CGT GAA TCC CGA AGC AGG CGG AGG	211
Ile Asp Arg Asp Asp Arg Asp Glu Arg Glu Ser Arg Ser Arg Arg Arg	
20 25 30 35	
GAC TCA GAT TAC AAA AGA TCT AGT GAT GAT CGG AGG GGT GAT AGA TAT	259
Asp Ser Asp Tyr Lys Arg Ser Ser Asp Asp Arg Arg Gly Asp Arg Tyr	
40 45 50	
GAT GAC TAC CGA GAC TAT GAC AGT CCA GAG AGA GAG CGT GAA AGA AGG	307
Asp Asp Tyr Arg Asp Tyr Asp Ser Pro Glu Arg Glu Arg Glu Arg Arg	
55 60 65	
AAC AGT GAC CGA TCC GAA GAT GGC TAC CAT TCA GAT GGT GAC TAT GGT	355
Asn Ser Asp Arg Ser Glu Asp Gly Tyr His Ser Asp Gly Asp Tyr Gly	
70 75 80	
GAG CAC GAC TAT AGG CAT GAC ATC AGT GAC GAG AGG GAG AGC AAG ACC	403
Glu His Asp Tyr Arg His Asp Ile Ser Asp Glu Arg Glu Ser Lys Thr	
85 90 95	
ATC ATG CTG CGC GGC CTT CCC ATC ACC ATC ACA GAG AGC GAT ATT CGA	451
Ile Met Leu Arg Gly Leu Pro Ile Thr Ile Thr Glu Ser Asp Ile Arg	
100 105 110 115	
GAA ATG ATG GAG TCC TTC GAA GGC CCT CAG CCT GCG GAT GTG AGG CTG	499
Glu Met Met Glu Ser Phe Glu Gly Pro Gln Pro Ala Asp Val Arg Leu	
120 125 130	
ATG AAG AGG AAA ACA GGT GAG AGC TTG CTT AGT TCC TGATATTATT	545
Met Lys Arg Lys Thr Gly Glu Ser Leu Leu Ser Ser	
135 140	
GTTCTCTTCC CCATCCCCAC CTAGTCCT AAAGAACATC CTGATCCCC CAGCTTCAA	605
GCACATGAAT TCAGAATGAA AGCTTGCCA TGGCTAAGGA ATGTGACTCT TTGAAAACCA	665
TGTTAGCATC TGAGGAACCTT TTAAACTT TGTTTAGGG ACTTTTTTTT CCTTAGGTA	725
GTAAATGATT ATAACACTCT TTTCCTTTTT TTGACTATAG TCGGTGCAAT GGTTACTTTA	785
AGCGTGAAT CAAATGGAGT GGCATTAGT TCAGGGGGCT TGTTCTTGC CATGGCAAAG	845
TATCAAGAAG ATCCCCAAGT CAAGTCACAT TTGTAAGCT GTTCCCCAAT TGGCTTGTG	905
ACCGAGTGTG GAAGCAGTGG GAGAGAGATT CACCTGTTAT AAAGGAACCTG ACTAACACAA	965
GTATCCCGTC TATATCTGAA TGCTGTCCT AGGTGTAAGC CGTGGTTTCG CCTTCGTGGA	1025
GTTTTATCAC TTGCAAGATG CTACCACTG GATGGAAGGCC AATCAGTTG CTTCACTCAC	1085
CAAGTCTAGA TATTCTGAA AATGGAACAA GTCTGTACAA TTAAAAAAA AGGTGAGG	1145
AGTGGTTGT TCCAAGGGAG TGACTTTTTT TTAAAAAAA AAGCTTGTAT TATTTAAAAA	1205
TTGATGTTAC TAGAATAAGT ACAGTACCAA GGACTTCATT ATAGAATTG TTCTGCCCTT	1265
AAACATGGCT ACCTACCTGG CAGGGCTTTG TTAACACTG AATACCTGTC TGGTATCAC	1325
TAAAACATCT TAATGTTCC CTTTTCTA GTTGTATA TTCTTATTAT GTCCATTGAG	1385
AGTAAGCTTA GTATATCAA CTCTCCATT GACAGTGAAG AGAACATAGT GAAAGTCTGT	1445

GGGGCATT	TTATAAGTAA	TTCCTTATT	TGCGCTGAAG	ACCAAAAGC	CTCCCTGGAGG	1505	
CGTA	ACTGCT	CAGACCGGT	TTCAGGGAT	ATTTAAGGAC	TTAGTGAAT	TTATGAACAA	1565
TAAGTCTGAT	GAGATTAGCC	TGGGAGTGTT	GTCCCGAGC	TGTCTAATCT	AGTTAGAGTG	1625	
GCATTAACAT	TCTAATCTCC	TTGAGAATG	CTTTTATAGT	CTGTC	AAAGCATTG	1685	
ATCGTTCTTC	GAGGTAGTGT	TAACTGAAGT	GTCTTCAGT	TGTC	AAAGAT AATGTCAGT	1745	
GCTTGGCACT	AAATAACAT	TTTTGCAAC	AACCTCAAGC	CACATTATG	AATGCC	1805	
ACCAAGTGC	TTCTGGGAAG	TTTGCTTGAC	TCATTATCTT	GCTTTCTGC	ACCATTCTGT	1865	
GATTGAGTC	ATCCATGAAT	CCATGAAATA	AACTTACATT	CTTGTGATGG	TAATATTGCC	1925	
ATTTATAACA	AGACTCACTA	ATGAGGGTAT	CACTTIGACT	GACTGATTTG	TAAAGTTT	1985	
TAAGGCTCTC	ATTTCTCAA	CCCAGAAATC	ACAGCCTGAT	TTTAA	TTAA GTAGAGCTTC	2045	
ATTCA	TACCATGAT	ACCATCCTAG	AAATCCAGA	ACATATACAA	GGTTCATG	2105	
AGTCTGTTT	CTTGACATGA	TAGCATGTT	TGATGCA	GATATGTCAG	AATGACTAAC	2165	
CTAGGAGTTT	AAAAACTCCTA	AGAAACTAAA	ACCTGTAAGA	CATTAAAG	TCTCCACAA	2225	
TTTAATGTAT	ACAAAGCTAT	GT	TTACTG	GTG AACACATTAC	AGTICA	2285	
ATAAAAGGCC	AGTAGGATTA	GGGACTCACT	GGTAGTTGG	AGTCT	CCAGCACACATCCC	2345	
TCCTAGTGGG	ATGATCTATT	CACATATCTC	CCAGC	TTTT	TGTGATATC	2405	
ACAGTIGAGT	GATGCC	CTT CAGCTT	TCTCC	TGGCC AGACATG	CCAG TCTT	2465	
AGATATGCA	GAGACAAAT	TCACAGCATG	TCTTAA	ATCTCAGGTTT	GCAAGAACCA	2525	
AATTGCTCAA	CA	GTATG	TTA GGTGAGGG	TTAGACTCC	TTTTAAAT CTGGATATCT	2585	
AACCACCTAC	TTAAATCTGT	TTGATAGTGT	CAAAC	CCACCC	CCACCTTGA TCC	2645	
CCCCAAAAAA	AAAAA	AAAAA	AAAAA	AAAAA	AAAAA AAAA	2689	

## SEQ ID NO:3

SEQUENCE LENGTH: 2981

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

CELL TYPE: leukocyte

SEQUENCE DESCRIPTION: SEQ ID NO:3

CCTCTCTCTC	TCTTTCAG	AGTCTTGCTC	TGTCGCCAG	GCTGGAGTGC	AGTGGCACAA	60
TCTCACTGCA	AGCTCCGCT	CCTGGGTTCA	CGCCATTCTC	CTGCTCAGC	CTCCAAATA	120
GCTGGGACAA	CAGGCACCTG	CCACCCAGCC	CGGCTAATT	TTTGTTTTT	TAGTAGAGAC	180
AGGGTTTCAC	CATGTTAGCC	AGGATGGCT	CAACTCTCTG	ACCTCGT	GAT CCACCCGCCT	240
CAGCCTCCA	AAGTGCTGAG	ATTACAGTG	TGAGCCACCA	CGCC	CAGCCA CATCTTCTT	300
TCTTCTTTT	TGGTTTTG	TTGTTGTTG	AGACAGGGTC	TGCTCTGTC	GCCTGGCTC	360
ACGTGAACCT	CCCACCTCAG	CTCTCCAAGT	AGCTGAGACC	ACAGG	TGTGA GCCACCA	420
CTGGGTAATG	TTTGTTTTT	TTTGTTAGAGA	TGGGTTCA	CCGTG	GCTGCC CAGACTGCTC	480
TCAAACCTCT	GGGCTCAAGT	GATCCACCTG	CCTTGACCTC	CTAAAGT	GCTG GCA GATTA	540
GTGTGAGCCA	CCGTGCTAG	CCGAGTGTCT	TTGTTATGTT	TCTGAGG	CAC GTGGATT	600
ATCTCTCTG	ATTCTCTGTT	CATCTCAGCC	TGTTGTTCC	ATTGAGATAA	ATGACTTTT	660
CTTGGTAACT	TAGAGTACTT	TGTTGTTA	CAGGTTAAC	CCTTATCA	TTATATCA	720

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TGCTGCATAC	TTTTCTTACA	TTTTCTTTT	CATTTAAAAA	ATTACATTGT	TTCATGAA	780
AGAATTTTA	AGTTTAAACG	TAGTCACCT	TGTCCATT	CTTATGACC	GGTCATT	840
AGGGCTTGT	TTAAGAAATC	GTCTTATC	CTGAGGTCA	AAAGATACTC	TACTGTATT	900
TCTTTAAGA	GCTGAAAAGG	TGTTTTAT	TTAATTATT	TGGGATTGGC	TTTGTGTGG	960
TGGGGATAAG	GATCACAA	TTATTTCATT	TTTTTCCAC	TGGTTATGC	CACTGGGCC	1020
ATTTCCATT	TTGAATAGT	CTTCTGTGC	AGAAAAGACT	TCACTAGCG	AGAACGCTG	1080
AGACTTACCC	TTCAAAAGGC	CCCATTACA	AGGCTAGCAC	TTGGCGTGA	TCTAGAAC	1140
TGGATTTGG	GGTGGTCCCT	ATAATGTGT	GTATGCTGA	CACCCACCTT	TCCTCTGGG	1200
AGTCTGAAAT	TTGGGTATAT	GTGGACAGA	GGCTGCCTAA	GTGACCGCT	TCAACAAACAG	1260
CCCTGGGTGC	TGGGTCACTC	ATGACCCATA	GACAAA	ATG CCA CAC	ATG TTG TCA	1314
				Met Pro His	Met Leu Ser	
				1	5	
CAG CTT ATT GCT CGA GGA GTT ACC ACA TCC TGT GTG ACT GCA CTG GGA						1362
Gln Leu Ile Ala Gly Gly Val Ser Thr Ser Cys Val Thr Ala Leu Gly						
10	15	20				
GAG GAA ACT CGT GCC TGG TTC CCT GTG TAT TTG TCC CAC GCC TCC AGT						1410
Glu Glu Thr Gly Ala Trp Phe Pro Val Tyr Leu Ser His Ala Ser Ser						
25	30	35				
CCC TTT GCT GAT CTC GTT TTT TGT CCT TTT GCT GAG ATA AAT CAC AGC						1458
Pro Phe Ala Asp Leu Val Phe Cys Pro Phe Ala Glu Ile Asn His Ser						
40	45	50				
CAG GAG TAT GAC AAT ATG CGG GGT CCT GTC AGT CCT CCT AAC AAA CAG						1506
Gln Glu Tyr Asp Asn Met Arg Gly Pro Val Ser Pro Pro Asn Lys Gln						
55	60	65	70			
TTC AAT CTG GGG GTG ATC TTT GGG ATC CCC AAC AAC TGT TGT CGT TTC CCC						1554
Phe Asn Leu Gly Val Ile Phe Gly Ile Pro Asn Asn Cys Arg Phe Pro						
75	80	85				
ACT GAT AAT AAA ATA ACT GAG AAG CAG CTA TTG GGC AAT GTT CTG AAC						1602
Thr Asp Asn Lys Ile Thr Glu Lys Gln Leu Leu Gly Asn Val Leu Asn						
90	95	100				
TAC CCT TGAACATTCA TGTCTTCATC TGAACATCCA TCTACTACCC CTGATTTTT						1658
Tyr Pro						
104						
CAGTGCAGGG TCCATATCCT GTATCACCA ATAATGGTC ATTGATCACCA ATAGGAAAGG						1718
AACAGTGAAA GCTCCACGGT GGTTGGAGG AAGGTGGCAG GCATTAGCG GTAACCTTT						1778
TGAGCAGATA GATTTATGT TTTGCAATG AGTGAATAA ATTTCCAT ATCTATTAA						1838
GGTTGGCAAT CATTATCTT TTATCATCTT GGAACATTG GAATTCTTT AATATGTTA						1898
GTTAGGAATT TTCTACCTTC CTACATCTGT CGGATAGTTT AAAATCCAC AGTTATTCA						1958
CGGGCTCCCT ATACCTGCCT GTGTGATTTC TAACATGTCA CGCTATGCAA CCAGTTGCTT						2018
TTACTTGAG AGTGTTCCTT TAGGTAATAG CTTATTATTG GTTATGAT TACAGTGTGT						2078
TAAAGACAGG TCJGTAGTTA TGTAAGAAT ATATCTATTI TTGCACTATT TTATTTATT						2138
ATATTTCTCT ATTCTATGTAT TTGTAAGAAT ATATCTATTI TTGCACTATT TTATTTATT						2198
ATTTTATTATTT ATTCTATGAA ACGGAGCCTT GTCTGTCA CTAGGCTGGA GTGCACTGGT						2258
GTGATCTCGA CTCACTGTGA CCTCCCCCTC CCAGGTTCAA GCGATTCTCC CGCCTCATCC						2318

TCCCAGTCA	TGGGATTAC	AGTCACGTGC	CATGAAGCCC	TGCTAATTTT	TGTATTTTT	2378
AGTAGAGACA	GGATTTCAC	ATGTTGGCGA	TGCTGGTTTC	GAACCTCTGG	TTTCAACTC	2438
CTGACCTCAA	GTGATCCACC	TGCCCTCGGCC	TCCCCAAAGAA	CTGGGATTAT	GGGCGTGAAC	2498
CACCAAGGCCA	GCTCAGTTTT	GCAGTGTTT	AAATACTGTT	GTCTTTGAGA	GGACAGAGGCC	2568
ACGCACATAG	ACTATGGTGA	TTACCATCAT	ATACTGGAAA	GTCCAAAGTC	TAGGCCAGTT	2618
AACTGTGAGC	CATCTCATCA	AACCTTAACA	GATGTCAT	TGTCCTATAA	AGGGGCTTCT	2678
GTCCCCATAGA	AATTCTATGTA	CCCAACCTAC	TCTTCAACCA	TGATTTTCTCT	CTGATGGCCT	2738
GTGTGAACAG	ATTAATGGTG	TCCATCTAAT	TCTTCCCA	CTGGGGAAA	GCAAATCATC	2798
AGGCCATTTG	CAAAAACTGC	TCTTGGTTGA	GCTTCTGCCT	TTAAATCATA	CCCAACAGTG	2858
ATGGCGTCCC	TTTATCAGCG	CTAATGACTC	TGACATCTCT	CTCCACTCAC	ATGTGAGGCC	2918
CCTCAGCTCT	CGATAAACAA	GTCTGTCTCG	GTTCATTTAT	TCTACAAAAA	AAAAAAAAAA	2978
AAA						2981

SEQ ID NO:4  
 SEQUENCE LENGTH: 1461  
 SEQUENCE TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 ORIGINAL SOURCE  
 ORGANISM: human  
 CELL TYPE: leukocyte  
 SEQUENCE DESCRIPTION: SEQ ID NO:4  
 AATTCCGGCAC GAGCAGCTTT CTAGTTCGAT TAGGCAACAG AATCCTTGAA ATGTGCTGT  
 GCACAGACCA GGTGGCTCTC TGGGCCAGTG TACTCTGAAA GATGTGCTGC CTGGCCCTAGC  
 TTGGTTCAGGA AAAGCAGGGC AAGCTTAGCC AAATCACACA TCTTGAAACAG CCCTCATTCG  
 TTATACTAAC TTTCACACCT TCTGGTGTGT ATAGGAGATA AAGATGCCAG ACGTGCTATT  
 AGGCTGCCAA TGGGACTGGG CTCGTATATC GTCTTCAAAT ATG AAT CAC CCC TGG  
 Met Asn His Pro Trp  
 1 5  
 CAT GTG TGT TTC CTG TTT AAG GTT CTC AGG TAT TAC CCA ACT GCA CCA  
 His Val Cys Phe Leu Phe Lys Val Leu Arg Tyr Tyr Pro Thr Ala Pro  
 10 15 20  
 ATA TTA AAA TCG ACA CAT ACC GTG TCA TGC AGT TGG TCC CGA ACT GTT  
 Ile Leu Lys Trp Thr His Thr Val Ser Cys Ser Trp Cys Arg Ser Val  
 25 30 35  
 TTA AGG GAA GTT GTC GGC AAT GTG AGT TTA TCA GAA AAC TTC ACC ATA  
 Leu Arg Glu Val Val Gly Asn Val Ser Leu Ser Glu Asn Phe Thr Ile  
 40 45 50  
 TCA GCA TTT TGC CCT GAG CTT ACA CCA TTC CCA GAT CAA GGT ACA AGC  
 Ser Ala Phe Cys Pro Glu Leu Thr Pro Phe Pro Asp Gln Gly Thr Ser  
 55 60 65  
 ACA ATG ATT TCC TTT CTT GAA AAG TTC AAC AAA AGC AAG AGA GAG AGA  
 Thr Met Ile Ser Phe Leu Glu Lys Phe Asn Lys Ser Lys Arg Glu Arg  
 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 1461

biosequences

70	75	80	85	
TTC GAG TTG ATG CTG CAT TTT TAT TCT GTG TTA AGT CTT GAA CCT GCT				584
Leu Glu Leu Met Leu His Phe Tyr Ser Val Leu Ser Leu Glu Pro Ala				
90	95	100		
GTT GCT GAA CAT TGG TCA GGG GAA TTT GAG AAG TCG AAA GTG GGC TTT				632
Val Ala Glu His Trp Ser Gly Glu Phe Glu Lys Trp Lys Val Gly Phe				
105	110	115		
TTT CAC CCT TTG AAA AGA GAG GAT GGA TTC TTC ACC AGA ACT GAC ATT				680
Phe His Pro Leu Lys Arg Glu Asp Gly Phe Phe Thr Arg Thr Asp Ile				
120	125	130		
TAAAAAAAAGT CAGCGTGGCA CGTTTAGTA TGTGTGGCAG ATCTAAASAG ACAATAATT				740
GATCTCAGGA GTGTTTATTTC TTGAACCATT TTCAGAACTC TAAGATTGA GAAATAATAA				800
AATATTGACC ATCCTCAA GAGAAAAACA CAGGGCGATC TTGGCATAG CCTGTCATT				860
TGCTCACATT TCACTCTCT CTCTCCAATC TCAGAGCCCC TTGCTGCCAA CAGGTGCTGT				920
GCTGGGTGGC AGGGGAGGTC TCTGGCTTT TTTTTTTTG ATCTCCGCT TAACATCTAG				980
CCTACTGGAG GAAGTGTATT TAATCATCCA CTTATCTGTAA ACAATTATC TCTGAGGGCC				1040
CGTCACATTC AGAGAAGATT CTAGGTTCTC TACAAGTATC CTCTCACTGT GTACATACTA				1100
AATCAACATC CTGCTGGATT TCCCCAGAC ATCTCCCTTC ATCACCATG GAGAGTATCC				1160
TCTAATTGCC AGCCCTATTTC ACCATACTCA TCTCATTTGA TCTGGAGTTT TCTGAGAGTG				1220
ACCGGGGGTG GGATGGACAG GATAATTAG CAAGAGTGTAA AGTAAAAT CTATATAATA				1280
AAAGTTATCT CCCTGTGCC CCCATGATCT ATTCTTTATG TAGCAGTCTG AATGAGATTT				1340
TCAGAACAA AACCAACTT ACCTAGTCT TTCTCTCTC TTCTCTCT 1400				
TTTTTTTAG TATTATGGCC AACAGAGCAA GACCCAGTCT CAGGAAAAAA AAAAAAAAAA				1460
A				1461

SEQ ID NO:5

SEQUENCE LENGTH: 3329

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

CELL TYPE: leukocyte

SEQUENCE DESCRIPTION: SEQ ID NO:5

CCAAAGTGCT GGGATTATAG GCATGAGCCA CTGGCCCCGG CCAGAATACC CTATCCTTAA	60
ACATGAAATT AGGGGAGGGG AGGACACAAAT TCAATCTATA ACAACTATCA CTGGCTGATT	120
TTGGCAGAGG CCTGTGGCCT CCAGTATTTC GAGGGAGCTG AGGGCCACTG ATCTCTCCAT	180
ATGCTCTCAA CATCATGGGA CTAGTAGGAT GAAAGCAAGC CTAGACCCAG ATTCTACCTC	240
AAGCAGGCAC ACAACATTC ATGCAGCTTC TACTTGGAGC CTGATGAAGT TCAAATTGTT	300
TGTCCCTCTGA GGCTCTCTTT GCATGGAAT TTCTCCCAGT ACAGATGAGA AAGTTCTGGG	360
GCAGCATTCA GCTTCTAGT TGGATTAGGC AACAGAAATCC TTGAAAATG TCTGTGCCACA	420
GACCAGGTGG CTCTCTGGGC CAGTGTACTC TGAAAGATGT GTGTCTGGC CTAGCTGGTT	480
GAGGAAAAGC AGGGCAAGCC TAGCCAATC ACACATCTG AACAGCCCTC ATTCCGTTATA	540

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CTAACCTTCC CACCCCTCTGG TGTGTATAGG AGATAAAAGT GGCAGACGTC CTATTAGGCT	600
GCAATGGGA GTGGGCTCTG ATATGGCTT TCAAAT ATG AAT CAC CCC TGG CAT	654
Met Asn His Pro Trp His	
1 5	
G TG TGT TTC CTG TTT AAG GTT CTC AGG TAT TAC CCA ACT GCA CCA ATA	702
Val Cys Phe Leu Phe Lys Val Leu Arg Tyr Tyr Pro Thr Ala Pro Ile	
10 15 20	
TTA AAA TGG ACA CAT ACC GTG TCA TGC AGT TGG TGC CGA AGT GTT TTA	750
Leu Lys Trp Thr His Thr Val Ser Cys Ser Trp Cys Arg Ser Val Leu	
25 30 35	
AGG GAA GTT GTA GGC AAT GTG AGT TTA TCA GAA AAC TTC ACC ATA TCA	798
Arg Glu Val Val Gly Asn Val Ser Leu Ser Glu Asn Phe Thr Ile Ser	
40 45 50	
GCA TTT TGC CCT GAG CTT ACA CCA TTC CCA GAT CAA GGT ACA AGC ACA	846
Ala Phe Cys Pro Glu Leu Thr Pro Phe Pro Asp Gln Gly Thr Ser Thr	
55 60 65	70
ATG ATT TCC TTT CTT GAA AAG TTC AAC AAA AGC AAG AGA GAG AGA TTG	894
Met Ile Ser Phe Leu Glu Lys Phe Asn Lys Ser Lys Arg Glu Arg Leu	
75 80 85	
GAG TTG ATG CTG CAT TTT TAT TCT GTG TTA AGT CTT GAA CCT GCT TTT	942
Glu Leu Met Leu His Phe Tyr Ser Val Leu Ser Leu Glu Pro Ala Phe	
90 95 100	
GCT GAA CAT TGG TCA GGG GAA TTT GAG AAG TGG AAA GTG GGC TTT TTT	990
Ala Glu His Trp Ser Gly Glu Phe Glu Lys Trp Lys Val Gly Phe Phe	
105 110 115	
CAC CCT TTG AAA AGA GAG .GAT GGA TTC ACC AGA ACT GAC ATT TAAAAA	1041
His Pro Leu Lys Arg Glu Asp Gly Phe Phe Thr Arg Thr Asp Ile	
120 125 130	
AAAGTCAGCGT GGCACGTTT AGTATGTGTG GCAGATCTAA AGAGACAATA TTTTGATCTC	1101
AGGAGTGT TTCTTGAAAC CATTTCAGA ACTCTAAAGT TTGAGAAATA ATAAAATATT	1161
GACCATCCTI CAAAGAGAAA AACACAGGGC GATCTTGGC ATAGCCTCTC ATTTTGTCTCA	1221
CATTTCACTT CTCTCTCTCC AACCTCAGAG CCCCTGCTGT GGAAACAGGTG CTGTGCTGGG	1281
TGGCAGGGGA GGTCTCTGGC TTTTTTTTTTG TGATCTCCGT CTTAACATCT AGCCTACTGG	1341
ACGAAGTGT A TTAATCATC CACTTAC TTAACATTA TCTCTGAGGG CCCCTCACAT	1401
TCAGAGAAGA TTCTAGGTTC TCTACAAGT TCCTCTCACT GTGTACATAC TAAATCAACA	1461
TCCTGCTGGA TTCCCCCAG ACATCTCCCT TCATCACCATT GGAGAGATG CCTCTAAATTG	1521
CCAGCCCTAT TCACCATACAT CACTCATT GATCTGGAGT TTCTGAGAG TGACGGGGG	1581
TGGCATGGAC AGGATAATTG AGCAAGAGTC TATAAGTAAATCTATATAA TAAAAGTTAT	1641
CTCCCTGTG CCCCCATGAT CTATCTTAA TGTAGCAGTC TGAATGGAGAT TTTCAGAAAC	1701
AAGAACCT TTAACCTTAGT CTCTCTCTCT TCTCTCTTCTT CTTTCTTTT CTTTTTTTTT	1761
AGTATTATGG GGATCTGTTT CTGTGTCCTCA GGGTGGACTG CAGTGGATG ATCTTGGCTC	1821
ACAGCAGCT TGAACCTCCC GGCTCAAGTG GTCTCTCTGC CTCTGCTTC CTTAGTAGCTA	1881
GGACTGCAAGG TTTGTGCCCCACACACCTGGC TAATTGAAAAA AAGAAATTTT TTTTCAATAG	1941
AGACAGTGTGCTTGTGATGTC CCCAGGGTGG TCTCAAACCTCCTGAA GTGATCCTC	2001

TGTCTCATCC	TCCCCAAAGTG	TTGGAATTAC	AGGTGTGAGC	TAATATACTC	GGCCAGTACC	2061
CTTCTAAAAA	CACTTCAGCA	CTTCCCCATTG	CACTGGGTT	GAAATTCCA	CCACTCACTG	2121
GGGCCACAA	GACTCTCAA	GACTGAATCC	TTGCTCAACA	TTG TGACCTG	CCCCCTACCA	2181
CCTGCAGCCT	CACTTGCCTG	GCTCCAGCCA	TGTGGATCTT	CTCTCTGTCT	CTAAAATGTC	2241
CTCAGGTCT	TTGCACCTGC	TGTTCTCCC	AAAGGCTGTG	TGATTCCAT	CAGTCAGTCT	2301
TAGCTCGTAT	ACCTCTTGG	AGACACCTCT	TCTGACCAAC	CAGTCCAAG	AATCTCTCT	2361
TATCATGTCA	CTCTGTTTTA	TTTATTATTT	TAGAGATGGA	GTCTCGCTCT	GTACCCAGG	2421
CTGGAGTGA	GTGGCGGAT	CTCTGCTCAC	TGCAAGCTCC	ACCTCTGGG	TTCATGCCGT	2481
TCTCTGCCCT	CAGCCCTCTG	AGTAACGGG	ACTATGGCA	CCCACCACTA	CACCCGGCTA	2541
ATTTTTGTA	TTTTTAGTGG	GGATGGGTT	TACTGTGT	AGCCAGGATG	GTCTTGATCT	2601
CCTGACCTG	TGATCTGCC	GCCTCCACCT	CCCCAAAGTG	TTTATTJATT	TTAAAGGCAT	2661
GTATCACTCT	CTGAAAATTA	GCTTCTTCT	TCTTTTTCT	IGTTATCATC	CATTTCCTCG	2721
AACCAAGATA	GAAGTTCTG	AGGCCAGAAC	TTCCTCTCT	CTGCCCTCA	CTATGTGTCT	2781
CTGGCACATA	CCCCAGTGC	TGCGCTCT	AAAGTAAAAT	CTTAGAAAT	ATTACTGTG	2841
ACTAAATAAA	TGAATAAATC	CCTTTAATG	CCCCTTGGA	AGTGTGCAAG	TAAGAATAG	2901
GATCCCTTTT	TAAGATTACA	CTTTGGCTA	TTGATCTGTG	TGTCTGGAAC	AAGATAACT	2961
TTGAAGATAC	TACCATGGG	CATGACATCA	TTGAGCTGA	TTAAGGTTT	AGTAATAAGA	3021
ATCCAGGATG	TGTCCGGGTG	CGGTGCTCAC	GCCTGTAATC	CTAGCATTT	GGGAGACCGA	3081
GGCGGGCAGA	TCACGAGGTC	AGCAGTTGA	GACCAGCTG	ACCAACATGG	TGAAACCCCG	3141
TCTCTACTAA	AAAATACAGA	AATTAGCCGG	GTGTGGTGT	GTCCACCTGT	AGTCCTAGCT	3201
ACTCAGGAGG	CTGGGGCAGG	AGAATTCTT	GAACCCGGGA	GGCGGAGGT	GCAGTGAGCC	3261
GAGATCACAC	CACTGCACTC	CAGCTGGC	AACAGAGCAA	GACCCAGTCT	CAGGAAAAAA	3321
AAAAAAAAA						3329

## SEQ ID NO:6

SEQUENCE LENGTH: 2276

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

CELL TYPE: leukocyte

SEQUENCE DESCRIPTION: SEQ ID NO:6

CTGAACTGGG	AGTCAGGGGG	TTGACTTTGTG	CCTGGCTGCA	GTAGCAGGGG	CATCTCCCTT	60										
GCACAGTTCT	CCTCTCGGC	CTGCCAAGA	GTCCACCAGG	CC	ATG GAC GCA GTG	114										
					Met Asp Ala Val											
					1											
GCT	GTG	TAT	CAT	GCC	AAA	ATC	AGC	AGG	GAA	ACC	GGC	GAG	AAG	CTC	CTG	162
Ala	Val	Tyr	His	Gly	Lys	Ile	Ser	Arg	Glu	Thr	Gly	Glu	Lys	Leu	Leu	
5						10				15			20			
CTT	GCC	ACT	GGG	CTG	GAT	GGC	AGC	TAT	TTG	CTG	AGG	GAC	AGC	GAG	AGC	210
Leu	Ala	Thr	Gly	Leu	Asp	Gly	Ser	Tyr	Leu	Leu	Arg	Asp	Ser	Glu	Ser	
25						30				35						

5' → 3' 3' ← 5'

GTG CCA CGC GTG TAC TGC CTA TGT GTG CTG TAT CAC GGT TAC ATT TAT Val Pro Gly Val Tyr Cys Leu Cys Val Leu Tyr His Gly Tyr Ile Tyr	258
40 45 50	
ACA TAC CGA CTG TCC CAG ACA GAA ACA GGT TCT TGG AGT GCT GAG ACA Thr Tyr Arg Val Ser Gln Thr Glu Thr Gly Ser Trp Ser Ala Glu Thr	306
55 60 65	
GCA CCT GGG GTA CAT AAA AGA TAT TTC CGG AAA ATA AAA AAT CTC ATT Ala Pro Gly Val His Lys Arg Tyr Phe Arg Lys Ile Lys Asn Leu Ile	354
70 75 80	
TCA GCA TTT CAG AAG CCA GAT CAA CGC ATT GTA ATA CCT CTG CAG TAT Ser Ala Phe Gln Lys Pro Asp Gln Gly Ile Val Ile Pro Leu Gln Tyr	402
85 90 95 100	
CCA GTT GAG AAG AAG TCC TCA GCT AGA AGT ACA CAA GGT ACT ACA GGG Pro Val Glu Lys Ser Ser Ala Arg Ser Thr Gln Gly Thr Thr Gly	450
105 110 115	
ATA AGA GAA GAT CCT GAT GTC TGC CTG AAA GCC CCA TGAAGAAAAA Ile Arg Glu Asp Pro Asp Val Cys Leu Lys Ala Pro	496
120 125	
TAAAACACCT TGTACTTTAT TTCTATAAT TAAATATAT GCTAAGTCCTT ATATATTGTA GATAATACAG TTCCGGTGAGC TACAAATGCA TTCTCTAACG CATTGAGTC CTGTAATGGAA	556
AGCATCTAGC ATGTCCTCAA AGCTGAAATG GACTTTGTAA CATACTGAGG AGCTTTGAAA	616
CGAGGATTGG GAAAAGTAAT TCCGTAGGTT ATTTTCAGTT ATTATATTAA CAAATGGGAA	676
ACAAAAGGAT ATGAAATACT TTATAAAGGA TTAATGTCAA TTCTGCCAA ATATAAATAA	736
AAATAATCCT CAGTTTTGTG GAAAAGCTCC ATTTTATGTC AAATATTATT TTATAGCTAC	796
TAATTTAAA ATGTCCTGCT TGATTTGATG GTGGGAAGTT GGCTGGTGTG CTTTGTCTTT	856
GCCAAGTTCT CCACTGCTA TGTTGTCATA GGCTCTTTTG GGATTTTIGA AGCTGTATAC	916
TGTGCTCAA AACAAAGCACT AACAAAGAG TGAAGGATTG ATGTTAATT CTGAAAGCAA	976
CCTTCTGCC TAGTCTTCTG ATATGGACA GTAAATCCA CAGACCAACC TGGAGTTGAA	1036
AATCTTATAA TTAAATAT GCTCTAAACA TGTTTATCGT ATTTGATGCT ACAGGATTG	1096
AAATTGTTT ACAAAATCCA TGAAATGAGT TTTCCTTTTC ATTACCTCT GCCCCAGTTG	1156
TTCTCTACTAC ATGGAAGACC TCATTTGAA GGAAATTTC AGCAGCTGCA GCTCATGAGT	1216
AACTGATTG TAACAAGCCT CCTTTAAAG TAACCTACA AAACCACTGG AAAGTTTATG	1276
GTGTATTAT TTAAATTTAA AATCCAAGT GATTGAAACT TACACGAGAT ACAGAATTTC	1336
ATGCGGCATT TTCTCTCAC ATTATATTT TTGTGATTT GTGATGGATT ATATGTCACT	1396
TTGCTACAGG GCTCACAGAA TTCACTCACT CAAACAAACAT AATAGGGCGC TGAGGGCATA	1456
GAAGTAAAAA CACCTGGTCC CTGCTCTAG TTCACTGCT TGTTGGACGA GAAAACAATA	1516
ACGATAAAAG ACAGTGAAG AAAATAACGA TAAAAGACAG TGAAAGAAAAA TAACAAATAA	1576
AGACAAAGGA AAAATAACAA TGAAAGTGA TAAGTACATG ATAAGCGAGG TTCCCCGTGT	1636
GTAGTAGAT CTGGCTTTA GAGGAGATA GATAAGTCAG TGCAAAACT CTGGTCCATG	1696
GGCCATATGA AAAGGCTAAG TTCACTGTA AAATAATAAC TGGGAATTCT GGTTGTGTA	1756
TGGGTGTTGG TGAACCTGGT TTAAATTAGT GAACTGCTGA GAGACAGAGC TATTCTCCAT	1816
GTACTGGCAA GACCTGATTT CTGAGCATT AATATGGATG CCGTGGGAGT ACAAAAGTGG	1876
AGTGTGGCCT GAGTAATGCA TTATGGGTGG TTACCATTT CTTGAGGTAA AAGCATCACA	1936
TGAACCTGTA AAGGAATTAA AAAATCCTAC TTCTATAATA AGTTGCATAG GTTAAATAAT	1996
	2056

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TTTTAATTAT ATGGCTTGAG TTTAAATTGT AATAAGCGTA ACTAATTATA	2116
GTTGTCATTC TGGATAATC CAAACATAT GAATTATGTT TGCATGTTCA CTTCCAAGAG	2176
CCTTTTTTGT AAAAAGCT TTTTGAAAT CATCAAGCTT TTACATTTA AATAAAGTGT	2236
TTGAAAGCTT TATTTAAAAA AAAAAAAA AAAAAAAA	2276

SEQ ID NO:7

SEQUENCE LENGTH: 165

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

CELL TYPE: leukocyte

SEQUENCE DESCRIPTION: SEQ ID NO:7

CACTTATAAA ATGTTAGGGC TTAATATTAT TCATAGATCG AGGATAGTTT CATTCTTAGT	60
---	----

CCCTCTCTTA GTCACTCTTC CTATACCAAT CTGACACCAT TTTACAATT AGAAAAGACA	120
--	-----

AATAACTGGT TGGGTACTT GATAGTATAA TAACC	155
---------------------------------------	-----

SEQ ID NO:8

SEQUENCE LENGTH: 278

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

CELL TYPE: leukocyte

SEQUENCE DESCRIPTION: SEQ ID NO:8

GAAGCAGAAC ATGAAACAGGT TAGAAAAGNT CNGCNNTCTG TTGGTGAAT CAAGGATCAA	60
---	----

GGGAAAGAGA CATTAAATTAA TCTCTGATACT ACCATTTGACT TGTCTCACCT TCAACCCCCAA	120
---	-----

AGGTCCATCC AGAAAATGGC TTCAAAAGAG GAATCTTCTA ATTCTAGTGA CAGTAAATCA	180
---	-----

CAGAGCCCGA GACATTTGTC AGCCAACGAA AGAAGGGAAA TGAAAAGAA AAAACTTCCA	240
--	-----

AGTGACTCAG GAGATTAGA AGCGTTAGAG GGAAAGGA	278
--	-----

SEQ ID NO:9

SEQUENCE LENGTH: 135

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

CELL TYPE: leukocyte

DRAFT DDBJ Sequence Database

SEQUENCE DESCRIPTION: SEQ ID NO:9  
TTCTGACAAT GAGTAAGAAG AAAGAGGGTC TTGCCCTTG GTTATTAAGA TTTATCATAG 60  
AGCAATAATA ASTAAATCG TGTTATACCA GCACAGACAT TAGACAAATA AACCAAGGGA 120  
CTGGACTAAA TAACC 135

SEQ ID NO:10  
SEQUENCE LENGTH: 197  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:10  
ATGGTACCCA GTTCAAATT AACATGGTA TTTACTTGT GTTCCCAAT TTAACATTAG 60  
GGAATTTTG GTTGTGGTC TGTTATCACT AGAAAAATAT ATATATTGGT GCTGAAGATA 120  
ATTTTGAGAT AATTAGACAA GACAGTTAG CATTACAAG AACAACTTG GCAGTTGAAG 180  
AATCTATTAA TATGACT 197

SEQ ID NO:11  
SEQUENCE LENGTH: 137  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:11  
CCACCGCACC TGGCTGATGC TTTCTATCT GACTCTTTC AGAGGACCT GAAAGACCT 60  
AACTGGAATC TTTCCTTGA GTCCTCCAAG CTAAACAAT TCTCTGGAA GATCACCTCT 120  
GTTCACTCCT GGTCTCT 137

SEQ ID NO:12  
SEQUENCE LENGTH: 274  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:12

CGTTTACAGA TTCTCTTGGG GCTGGCGGTG GAACTACAAA GGGATCCGGTG CCTATATCAC 60  
AATACCAAC TTGATAATAA TCTAGATCT GTGTYTCIGC TTATAGACCA TGTTTGTAGT 120  
ACGTAAGAGG AAAACTTCCT ATATTCGAA ACAGCTAAC ATTTCACAAA ATTTTAGTTT 180  
TCTTTTTAG AGTCTTATCC TGTAGCTATA TAACAGTTCA TGTCTGATTG AGCATTGTT 240  
CACGAGTAAA GCTGGAACTA TGAAAATTGA AAAT 274

SEQ ID NO:13  
SEQUENCE LENGTH: 171  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:13  
GATTAGGTGA CCTTCCTTGA ARAGCCACGG GTTCCCATA TCGAAATGCT ATTCAATTACC 60  
CGACTCACCT ANGTCTTAC AAAGGAAGCG AGAAAATTGC TTGTTGGG CCATGCCCT 120  
TTTGCANAGG TTCCTAAGTA TAGTCGCCAN AATTTTTTA ATGGCCTAAA G 171

SEQ ID NO:14  
SEQUENCE LENGTH: 161  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:14  
AGGGGGCTT GTTCTGCCT CAGCACATTG GTTACACCCG TCAGGTGGTG GCGATGACTT 60  
AATTCTAGC CCAAGAAGAA TATAATGTTA AAACCTGGTTA TGAAATTTT GTGCCCTCTCC 120  
TTTTAATGC AGTATTTAGT TCAGATGTTG GCGATTTTC A 161

SEQ ID NO:15  
SEQUENCE LENGTH: 323  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:15

TATAAGGWWG GAACTTACT ATCTCTAATG ACCTTACTG TGCTGACTTT AATACTCTGT 60  
GAAGGTTAGA GTTCAGTCAA TGTTACCTAG AAACAGCCCC CGCTCTGGAA TACTTTATTC 120  
TTAGCCCTAT ATTGGGGTT TGGATGTCCA CTGTGCTGGT TCCCAGAGAT AGTAAGGGGA 180  
TGAGACTATT GGTTACATCT CCTGACCCAC ATACTTAAGA TCCAGATGAA CAAGACACTT 240  
TTCACTCTG CTTGGTAGAA CCTATTGTYK SHAGGAACA GYTCTAAAG AATGGTTCTA 300  
GCCAGACCT GTCCGYACCA GAA 323

SEQ ID NO:16  
SEQUENCE LENGTH: 138  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:16  
ATGATGCAA ATAGTTCTG CCTGATTGGT GAGATTTGGG ATGGGGCCCC ACTTTGTTTC 60  
TCTTTCTGCA TAAAAATTTC AACATTTTA CAAAATTTTC AAAAACTTCT CCTCAGTCTG 120  
TACATCTTG TTAATCG 138

SEQ ID NO:17  
SEQUENCE LENGTH: 135  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:17  
TGATCCCCAC AATTCTTGT GATTGGTGAG GAACTATAAA TGACTCCCAT CCAAGCTTAT 60  
ACCAGAAAAA AGGAGCACAT TTCTACAAA TTATATCATI TTTAATCCAT TACCACATTA 120  
TTTAAAGGGGA ACTAC 135

SEQ ID NO:18  
SEQUENCE LENGTH: 219  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte

GB/T 9388.1-2008

SEQUENCE DESCRIPTION: SEQ ID NO:18  
CTGAGAGGAG CCATGTATAAC AACCACTTT TCTAACATG GTCTTATTAA AACTTGAAT 60  
ATAAGTACAC CTGCTCGAAG TGTTCATCTA TATTATTAA GAACAAGCAA CTGTAAAACA 120  
GTAAAATCAC AAAAGGTAAG TTGTTGGAAG ACAACAAAAA AGAATTACTA TATCTGATCC 180  
TGCCTGTTTA TTTAGAATC TGTTAATAGG CCTACAGCT 219

SEQ ID NO:19  
SEQUENCE LENGTH: 191  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:19  
ACAGTGAGTG TGGCTGAAAC CTAAGCTGAA GGAAGGGAGG AGCAGGGACT GCCATGAGGG 60  
GTCCTGGAC AGAAACTCTT CAGCAGGCC TGAAGTTAG TTCAGGGCT ACATGGAATA 120  
CCACTATTAA GCACACAGGT GTGATCTGAG GTGAGGGACT ACCTTTGGA TCTTGGTTT 180  
CTCATTTATT T 191

SEQ ID NO:20  
SEQUENCE LENGTH: 148  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:20  
CTGGAGGTGA AGGGAAGGAA AGAAAAGGAA AACTATCTAC CTGGCAGGAA AAGAGATAAG 60  
CTCCCAAGAA CACCAAAGCA GATGATGAGT CTAGCTCTAC CCAGCCTTCC TCCCCACGAA 120  
TCCAGATCAT AGTAAGAAAC TCTGGGCT 148

SEQ ID NO:21  
SEQUENCE LENGTH: 306  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte

SEQUENCE DESCRIPTION: SEQ ID NO:21

CCACCAACAG AAATGAAACAA AAAGCATTTC ACCTAAAAAT ACACCCAGCAA AATGTACTCA 60  
GCTTCAATCA CAAATACGAC TCTTAAAC CGCAGAAATT TCTCAACAC TCAGCCTTA 120  
TCACTCAGCT GGATTTTC CTTCAACAAT CACTACTCCA AGCATTGGGG AACACAACCTT 180  
TTAATCATAC TCCAGTGTT TCACAAATGCA TTCTAATAGC ACCGGGGATCA GAACAGTACT 240  
GCATTTACTT GCCAACAGAA CAGACAGACC TGAAGTCAAG ACAACTGCAT TCTCTGTGAA 300  
GTCTGT 306

SEQ ID NO:22

SEQUENCE LENGTH: 357

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

CELL TYPE: leukocyte

SEQUENCE DESCRIPTION: SEQ ID NO:22

GTAGCATTTC GGCAGAACCA TTGTTAATTAA AAGGGACTTY TGGACCGCAA CYTTAATGTA 60  
CCAGATTATT GAGCRGCCCA ATGAATGCTT CATTCTCATT GTTTAAGGTG CTGCTTTGAT 120  
TTTTTTCA ATTCTTGTAA CTATTTTTA TTTTTGGAG AGGCACATCC CCAAATTGG 180  
ATGAGGTATT TGTTGATAAA TAATTCAATCA ATTTCCACAA TGCAAGACAAA AATGCTGCC 240  
CAGAGTGGAA AAATAAAACA AGGGGGAGAA GAGTTGAGT AACGGAGAAG TTCTGTGGAA 300  
TCCTAGTGAC AAAAGTTGAG AACTACCTT TAAATAAGAC AGTGAGGTA CAAATCT 357

SEQ ID NO:23

SEQUENCE LENGTH: 219

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

CELL TYPE: leukocyte

SEQUENCE DESCRIPTION: SEQ ID NO:23

TGGAATAGCC AGGAGAATTG TGGAAAAGTA GAATAATGAG GTAGGGCTTC CCTTCGCTAT 60  
TTTGAAGTGC AGATTCACT ATGTAACACC ATTAGGAACG GGCACGTGAA TAGACAGATC 120  
AATAGTTAACT AGCTGTATTA GCCAGAAAAT GTGTAAAGGA CAACAGGCTA ACTAACCCCTG 180  
TCACTGTAA TCTAAAATT AAGCTCTAGAT AGAGTCCTC 219

SEQ ID NO:24

SEQUENCE LENGTH: 251

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:24  
TGAAAGGGGA ATAGAACGAC AAGAGTCAGT AATCAATAAC AAACAACCTCA AGGTGCTCTC 60  
TCCTTACACT GGTGTTCCCC AAAGTGAGGT GAATTGCCAG CCACGTGGAG TCAGGGCCAG 120  
TTACATAAGA CATTCTCGGT AAGCCCCCTT TGGGTATCCC AAATAAGGAC TGGGGTCCGGT 180  
TTATGTGTAG TCCATTATTA ACAACTAAAC GAACAAACCT AGTGAATTGC AATAATTCA 240  
CACCACACAGA A 251

SEQ ID NO:25  
SEQUENCE LENGTH: 233  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:25  
GTGAAAGAG TCTTGGAG GCTTTAGAC CAAACCCCTC TGATGCTCA ARCTTGGGT 60  
ACAGGATTC TAAGAAGTGG AACAGTCTCC AGGGGTGTCG ARCTCATCGC TCAAGGCAGG 120  
TTATCTTATC TGAATAATTG TGCTGTGCA CTATGGGAT AGTTCTCCTT CAGATGAGCT 180  
GAAATTTCT CCATAGCTTC CTCTATTAAA CCCAATTCCA CTTCTCAGGG TCA 233

SEQ ID NO:26  
SEQUENCE LENGTH: 176  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:26  
CAAAAGCGCT GAAGTTAACG ATTAATACCG CAGATTATGC ATTATATGATC AGTATCCAAA 60  
ACTCCAACTA CAAACAAATGC AAAGTACTGTC TCTCTAGTAT TATTTTTGCA ATTGTACTA 120  
ATGTTAACGA TCAAGGGAAA TAAAACACAT CATTGCAACAT TACAGCCGCA AAAAAC 176

SEQ ID NO:27  
SEQUENCE LENGTH: 241  
SEQUENCE TYPE: nucleic acid

DNA sequence analysis

STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:27  
AGAGAGTAAA GCAAGCTATT TTGACAGCAA CCTAATAACA GCTGCTCTCT TCCACTCTT 60  
GGCTAACTCA TCCCCAGAT AGCCTCTTT TCTCTTATCA ATTCCCTGTT GCAACAATAA 120  
TAAATGCCAC ACCTGATGGA GTCATCTAGGC ACTTTCTTAG TGACAAGTGC CTAGGACAGA 180  
GGAGAAAACA AAGAACACT GACAACCCT GAAAACGTAC ATATCAGGCC AGGCATGTCA 240  
C 241

SEQ ID NO:28  
SEQUENCE LENGTH: 217  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:28  
GCTCGAGAGG TGGTGATGTT GCTGAATAAT TGCTTTTAA AGCTGGAGGG GACTTCCAAG 60  
AGTCTCTCAT TTAAGAARAA AAATTAAGA CATAATTGGT AACGGTTTG ACTGCTCCAG 120  
AGCCAACACT TTGCTCACAA TCCTACAGAT CTACTTCACC TGTAACTACA ATTTTCCTGA 180  
AGACATAGAA GAAAATCAA TTGTTCTAAT CCATATG 217

SEQ ID NO:29  
SEQUENCE LENGTH: 233  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:29  
AATCTTAGCA TAATGCTTCC TGGGAAATTG TGAAATTGAT TCCATTCTG CGTTTACAAA 60  
CACACACGAA GTTCTCTAGTT CACTGGACT TCCTGATTG TTCTTITAGC TTGCTCCCTTC 120  
TCACCTAGAA GCTCTGTTA TTCTGAGCA ACCCTGGGGC TTGTCICATA GGACAGGATT 180  
TATTTATCTC ATCAAGGCTG AGTGTGCCTT AGGAAGTCAT AAACATAAAA AGA 233

SEQ ID NO:30

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SEQUENCE LENGTH: 228  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:30  
TATAGACAGG GTAGGGACGA TTAGCCCTC GACAACTTT CACAAATAA CACACGTTA 60  
ACTACCTCTC AGGTCAATGAT AAAGACCGGC CGGGCAGAAA CACTGTAATC CCAGCTACTC 120  
GGGAGCCTGA GGCAATGAGAA TCACTTGAAC CTGGGAGGTG GAGGTTGCCA TGAGCCGAGA 180  
TCACCCATT GCACACTACAGC AGAGTCAAAC TCCATCTG 228

SEQ ID NO:31  
SEQUENCE LENGTH: 298  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:31  
GCTTATGATT ACAAACATCC CTATCATATGAA AATCTCAGCA TTTCATGGCT GCTGCGTTCA 60  
ATCGCTTTTG CTGAAATAGG TATCCCTTGA TGTCGACTAT TTGATTTCA CGAGTCGTT 120  
CTCTCTGGCA GTGCTCCCTG CAAATGTGTC CTTTCAGAA AACAAACCT GCAAGTGCT 180  
TGTAATGTAC CATGACCTTA TCATGTGAAG GACAATGGC TCTTGTGCTT ATTAGATAGC 240  
AGATGAAC TGAGTAACTGAA TTCTTGGTCT GAAGCTTGA TAAGGTAGA TGTCTTGTG 298

SEQ ID NO:32  
SEQUENCE LENGTH: 291  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:32  
ACTTCGAAGG GAAAAAGAGG AAGGAAAAGG ACTGTTAATA AAATAACAAA GGCAGCAATC 60  
AGAATGAACC AGAGCCAGGA CAGCGTAAAG GCTAGGTCA CAGTGAGATG AAAGAACCTG 120  
AAAACAAGTT TAAAACCTAA AAGAGGTTA TTCTCAAGTT ATACTACAGT GAAAAACAT 180  
GAAAAAACAC AAAAAGGACA GGCATAAAGG CACAGGCATA CATAACAAGGC AAATTTAAC 240

ACAATATTTA CTTGCAAAAG AGCCACAGA GACATGTCAA TGAAGTCATA G

291

SEQ ID NO:33

SEQUENCE LENGTH: 230

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE

ORGANISM: human

CELL TYPE: leukocyte

SEQUENCE DESCRIPTION: SEQ ID NO:33

Met Glu Asp Gly Phe Leu Asp Asp Gly Arg Gly Asp Gln Pro Leu His  
1 5 10 15  
Ser Gly Leu Gly Ser Pro His Cys Phe Ser His Gln Asn Gly Glu Arg  
20 25 30  
Val Glu Arg Tyr Ser Arg Lys Val Phe Val Gly Gly Leu Pro Pro Asp  
35 40 45  
Ile Asp Glu Asp Glu Ile Thr Ala Ser Phe Arg Arg Phe Gly Pro Leu  
50 55 60  
Ile Val Asp Trp Pro His Lys Ala Glu Ser Lys Ser Tyr Phe Pro Pro  
65 70 75 80  
Lys Gly Tyr Ala Phe Leu Leu Phe Gln Asp Glu Ser Ser Val Gln Ala  
85 90 95  
Leu Ile Asp Ala Cys Ile Glu Glu Asp Gly Lys Leu Tyr Leu Cys Val  
100 105 110  
Ser Ser Pro Thr Ile Lys Asp Lys Pro Val Gln Ile Arg Pro Trp Asn  
115 120 125  
Leu Ser Asp Ser Asp Phe Val Met Asp Gly Ser Gln Pro Leu Asp Pro  
130 135 140  
Arg Lys Thr Ile Phe Val Gly Val Pro Arg Pro Leu Arg Ala Val  
145 150 155 160  
Glu Leu Ala Met Val Met Asp Arg Leu Tyr Gly Gly Val Cys Tyr Ala  
165 170 175  
Gly Ile Asp Thr Asp Pro Glu Leu Lys Tyr Pro Lys Gly Ala Gly Arg  
180 185 190  
Val Ala Phe Ser Asn Gln Gln Ser Tyr Ile Ala Ala Ile Ser Ala Arg  
195 200 205  
Phe Val Gln Leu Gln His Gly Glu Ile Asp Lys Arg Val Ser Leu Ile  
210 215 220  
Leu His Phe Gly Lys Phe  
225 230

SEQ ID NO:34

SEQUENCE LENGTH: 143

SEQUENCE TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:34  
Met Gly Ser Asp Lys Arg Val Ser Arg Thr Glu Arg Ser Gly Arg Tyr  
1 5 10 15  
Gly Ser Ile Ile Asp Arg Asp Asp Arg Asp Glu Arg Glu Ser Arg Ser  
20 25 30  
Arg Arg Arg Asp Ser Asp Tyr Lys Arg Ser Ser Asp Asp Arg Arg Gly  
35 40 45  
Asp Arg Tyr Asp Asp Tyr Arg Asp Tyr Asp Ser Pro Glu Arg Glu Arg  
50 55 60  
Glu Arg Arg Asn Ser Asp Arg Ser Glu Asp Gly Tyr His Ser Asp Gly  
65 70 75 80  
Asp Tyr Gly Glu His Asp Tyr Arg His Asp Ile Ser Asp Glu Arg Glu  
85 90 95  
Ser Lys Thr Ile Met Leu Arg Gly Leu Pro Ile Thr Ile Thr Glu Ser  
100 105 110  
Asp Ile Arg Glu Met Met Glu Ser Phe Glu Gly Pro Gln Pro Ala Asp  
115 120 125  
Val Arg Leu Met Lys Arg Lys Thr Gly Glu Ser Leu Leu Ser Ser  
130 135 140 143

SEQ ID NO:35  
SEQUENCE LENGTH: 104  
SEQUENCE TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:35  
Met Pro His Met Leu Ser Gln Leu Ile Ala Gly Gly Val Ser Thr Ser  
1 5 10 15  
Cys Val Thr Ala Leu Gly Glu Glu Thr Gly Ala Trp Phe Pro Val Tyr  
20 25 30  
Leu Ser His Ala Ser Ser Pro Phe Ala Asp Leu Val Phe Cys Pro Phe  
35 40 45  
Ala Glu Ile Asn His Ser Gln Glu Tyr Asp Asn Met Arg Gly Pro Val  
50 55 60  
Ser Pro Pro Asn Lys Gln Phe Asn Leu Gly Val Ile Phe Gly Ile Pro

65                   70                   75                   80  
Asn Asn Cys Arg Phe Pro Thr Asp Asn Lys Ile Thr Glu Lys Gln Leu  
              85                   90                   95  
Leu Gly Asn Val Leu Asn Tyr Pro  
              100

SEQ ID NO:36  
SEQUENCE LENGTH: 133  
SEQUENCE TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:36  
Met Asn His Pro Trp His Val Cys Phe Leu Phe Lys Val Leu Arg Tyr  
    1                5                10                15  
Tyr Pro Thr Ala Pro Ile Leu Lys Trp Thr His Thr Val Ser Cys Ser  
    20                25                30  
Trp Cys Arg Ser Val Leu Arg Glu Val Val Gly Asn Val Ser Leu Ser  
    35                40                45  
Glu Asn Phe Thr Ile Ser Ala Phe Cys Pro Glu Leu Thr Pro Phe Pro  
    50                55                60  
Asp Gln Gly Thr Ser Thr Met Ile Ser Phe Leu Glu Lys Phe Asn Lys  
    65                70                75                80  
Ser Lys Arg Glu Arg Leu Glu Leu Met Leu His Phe Tyr Ser Val Leu  
    85                90                95  
Ser Leu Glu Pro Ala Val Ala Glu His Trp Ser Gly Glu Phe Glu Lys  
    100              105              110  
Trp Lys Val Gly Phe Phe His Pro Leu Lys Arg Glu Asp Gly Phe Phe  
    115              120              125  
Thr Arg Thr Asp Ile  
    130

SEQ ID NO:37  
SEQUENCE LENGTH: 133  
SEQUENCE TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:37  
Met Asn His Pro Trp His Val Cys Phe Leu Phe Lys Val Leu Arg Tyr

1	5	10	15
Tyr Pro Thr Ala Pro Ile Leu Lys Trp Thr His Thr Val Ser Cys Ser			
20	25	30	
Trp Cys Arg Ser Val Leu Arg Glu Val Val Gly Asn Val Ser Leu Ser			
35	40	45	
Glu Asn Phe Thr Ile Ser Ala Phe Cys Pro Glu Leu Thr Pro Phe Pro			
50	55	60	
Asp Gln Gly Thr Ser Thr Met Ile Ser Phe Leu Glu Lys Phe Asn Lys			
65	70	75	80
Ser Lys Arg Glu Arg Leu Glu Leu Met Leu His Phe Tyr Ser Val Leu			
85	90	95	
Ser Leu Glu Pro Ala Phe Ala Glu His Trp Ser Gly Glu Phe Glu Lys			
100	105	110	
Trp Lys Val Gly Phe Phe His Pro Leu Lys Arg Glu Asp Gly Phe Phe			
115	120	125	
Thr Arg Thr Asp Ile			
130			

SEQ ID NO:38

SEQUENCE LENGTH: 128

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE

ORGANISM: human

CELL TYPE: leukocyte

SEQUENCE DESCRIPTION: SEQ ID NO:38

1	5	10	15
Met Asp Ala Val Ala Val Tyr His Gly Lys Ile Ser Arg Glu Thr Gly			
20	25	30	
Glu Lys Leu Leu Leu Ala Thr Gly Leu Asp Gly Ser Tyr Leu Leu Arg			
35	40	45	
Asp Ser Glu Ser Val Pro Gly Val Tyr Cys Leu Cys Val Leu Tyr His			
50	55	60	
Gly Tyr Ile Tyr Thr Tyr Arg Val Ser Gln Thr Glu Thr Gly Ser Trp			
65	70	75	80
Ser Ala Glu Thr Ala Pro Gly Val His Lys Arg Tyr Phe Arg Lys Ile			
85	90	95	
Lys Asn Leu Ile Ser Ala Phe Gln Lys Pro Asp Gln Gly Ile Val Ile			
100	105	110	
Pro Leu Gln Tyr Pro Val Glu Lys Lys Ser Ser Ala Arg Ser Thr Gln			
115	120	125	
Gly Thr Thr Gly Ile Arg Glu Asp Pro Asp Val Cys Leu Lys Ala Pro			

**SEQ ID NO:39**  
 SEQUENCE LENGTH: 305  
 SEQUENCE TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 ORIGINAL SOURCE  
 ORGANISM: human  
 CELL TYPE: leukocyte  
 SEQUENCE DESCRIPTION: SEQ ID NO:39  

TCTGAACTG AAGCCAATG TTTAGACTAG AATGTTATGA GATTAAACCC ACNNNNNNNTT	60
ATTACATAGAC ATAAACCCCTC ATTTTAATTAA CTGGATCTGG ATTTTGTCATATGTTGGAAAT	120
CATAATTAA ACAAAATCAA CTAAGATGAT CCAAGTTCCA CACAATGCA CTTCAATATT	180
CAACTCCGTG TGAAGATGCC TGACTACTGC GTCACAAAGAT TCTGAGGTGT CGTAAAAGC	240
CTGGCTCGTG GTTTCATATT ATAGTGACATGTTGGGT TATAATCACA AACCTGGAAC	300
TCTGT	305

  
**SEQ ID NO:40**  
 SEQUENCE LENGTH: 256  
 SEQUENCE TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 ORIGINAL SOURCE  
 ORGANISM: human  
 CELL TYPE: leukocyte  
 SEQUENCE DESCRIPTION: SEQ ID NO:40  

GAAACCACGG CTTACACCTA GAGACAGCAT TCAGATATAG ACGGGATACT TGTGTTAGTC	60
AGTTCCCTTA TAACAGGTGA ATCTCTCTCC CACTGCTTCACACTGCGTG ACAAAAGCAA	120
TTGGGAAGCA GCTTTACAAA TGTGACTTGA CTTGGGGATC TTCTTGATAC TTGGCCATGG	180
CAAGGAACAA GCCCCCTGAA CAAATGCCA CTCCATTGA TTCCACCCCTT AAAGTAACCA	240
TGCAACCGAC TATACT	256

  
**SEQ ID NO:41**  
 SEQUENCE LENGTH: 244  
 SEQUENCE TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 ORIGINAL SOURCE  
 ORGANISM: human  
 CELL TYPE: leukocyte  
 SEQUENCE DESCRIPTION: SEQ ID NO:41  

TACTCTCAA CCATGATTTT TCTCTGATGG CCTGTGGAAC CAGATTAATG GTGTCCATCT	60
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Sequence Listing

AATTCCTTCC CCACTGGGG AAAGCAAATC ATCAGGCCA TTGAAAAAC TGCTCTGGT  
TGAGCTTCT GCCTTAAATC ATACCCACAG TGAATGGGT CCCTTATCA CCGCTAATGA  
CTCTGACATC TCTCTCCACT CACATGTGAG CCTCCCTCAGC TCTCGANAAA CAAGTCNGTC  
TCGG 120  
180  
240  
244

SEQ ID NO:42  
SEQUENCE LENGTH: 258  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:42  
TCTCAGAAA CTCCAGATCA AATGAGATGA GTATGGTGNM NAGGGCTGGC AATTAGAGGA 60  
TACTCTCCAA TGGTGTGAA GGGAGATGTC TGGGGAAAT CCAGCAGGAT GTTGATTTAG 120  
TATGTCACACA GTGAGAGGAT ACTTGTAGAG AACCTAGAAT CTTCTCTGAA TGTGACGGGC 180  
CCTCAGAGAT AATTGTTAAC AGATAAGTGG ATGATTAAT ACACCTCCTC CAGTAGGCTA 240  
GATGTTAAGA CGGAGATC 258

SEQ ID NO:43  
SEQUENCE LENGTH: 26  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:43  
GGGCTTAATA TTATTCTAG ATCGAG 26

SEQ ID NO:44  
SEQUENCE LENGTH: 26  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:44  
GTTATTATAC TATCAAGTAA CCCAAC 26

SEQ ID NO:45  
SEQUENCE LENGTH: 25  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

biosequences

MOLECULE TYPE: other nucleic acid, synthetic DNA SEQUENCE DESCRIPTION: SEQ ID NO:45 CTGGATCTGG ATTTTGTCATATGCT	25
SEQ ID NO:46 SEQUENCE LENGTH: 25 SEQUENCE TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: other nucleic acid, synthetic DNA SEQUENCE DESCRIPTION: SEQ ID NO:46 GTTTGTGATT ATAACCCAAC ATGTC	25
SEQ ID NO:47 SEQUENCE LENGTH: 25 SEQUENCE TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: other nucleic acid, synthetic DNA SEQUENCE DESCRIPTION: SEQ ID NO:47 GAAGGGGAAG AGACATTAATTTATC	25
SEQ ID NO:48 SEQUENCE LENGTH: 24 SEQUENCE TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: other nucleic acid, synthetic DNA SEQUENCE DESCRIPTION: SEQ ID NO:48 GCTTCTAAAT CTCCGTAGTC ACTT	24
SEQ ID NO:49 SEQUENCE LENGTH: 24 SEQUENCE TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: other nucleic acid, synthetic DNA SEQUENCE DESCRIPTION: SEQ ID NO:49 GACAATGAGT AAGAAGAAAG AGCG	24
SEQ ID NO:50 SEQUENCE LENGTH: 24 SEQUENCE TYPE: nucleic acid STRANDEDNESS: single	

TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:50  
GTCCAGTCCC TTGGTTTATT TGTG

24

SEQ ID NO:51  
SEQUENCE LENGTH: 25  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:51  
GGTACCCAGT TTCAAATTAA CATGG

25

SEQ ID NO:52  
SEQUENCE LENGTH: 25  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:52  
GATTCTTCAA CTGCCAACT TGTTC

25

SEQ ID NO:53  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:53  
GCTGATGCTT TTCTATCTGA CTTC

24

SEQ ID NO:54  
SEQUENCE LENGTH: 22  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:54  
GACCAGGACT GAACAGAGGT GA

22

SEQ ID NO:55  
SEQUENCE LENGTH: 25  
SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:55  
GCTTATAGAC CATGTTGTA GTAGG 25

SEQ ID NO:56  
SEQUENCE LENGTH: 25  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:56  
GTGAACAAT GCTAAATCAG ACATG 25

SEQ ID NO:57  
SEQUENCE LENGTH: 22  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:57  
GCCACGGGTT TCCCATATCG AA 22

SEQ ID NO:58  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:58  
GACTATACTT AGGAACCTCT GCAA 24

SEQ ID NO:59  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:59  
GTTCTGCTCT CAGCAGATTG GTTA 24

SEQ ID NO:60  
SEQUENCE LENGTH: 24

BIOCHIEMISTRY

SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:60  
GCCAACATCT GAACTAAATA CTGC

24

SEQ ID NO:61  
SEQUENCE LENGTH: 26  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:61  
GTTCA GTGAA TGTTACCTAG AAACA

25

SEQ ID NO:62  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:62  
GGAGTGAAA CTGTCTTGT CATC

24

SEQ ID NO:63  
SEQUENCE LENGTH: 25  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:63  
GTATGACAAA TAGTTCTGC CTGAT

25

SEQ ID NO:64  
SEQUENCE LENGTH: 25  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:64  
GATTAACAAA GATGTACAGA CTGAG

25

SEQ ID NO:65

SGAAGGATG TCAAGATAG ACCG

SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:65  
GAGACAGCAT TCAGATATAG ACCG

24

SEQ ID NO:66  
SEQUENCE LENGTH: 22  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:66  
GGGTGGAATC AAATGGAGTG GC

22

SEQ ID NO:67  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:67  
GATGGCCTGT GTGAAACAGAT TAAT

24

SEQ ID NO:68  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:68  
GAGAGAGATG TCAGACTCAT TAGC

24

SEQ ID NO:69  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:69  
GATCCCCACA ATTCTTGTG ATTC

24

SEQ ID NO:70  
SEQUENCE LENGTH: 25  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:70  
GTTCCCTAA ATAATGTGG TAATG 25

SEQ ID NO:71  
SEQUENCE LENGTH: 23  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:71  
GAGGATACTC TCCAATGGTG ATG 23

SEQ ID NO:72  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:72  
GTCTAACAT CTAGCCTACT GGAG 24

SEQ ID NO:73  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:73  
GAGAGGAGCC ATGTATACAA ACCA 24

SEQ ID NO:74  
SEQUENCE LENGTH: 26  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:74  
GCACCGAGGA TCAGATATAG TAATT 26

SEQ ID NO:75  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:75  
GCTGAAACCT AAGCTGAAGG AAGG

24

SEQ ID NO:76  
SEQUENCE LENGTH: 22  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:76  
GTCCTCACC TCAGATCACA CC

22

SEQ ID NO:77  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:77  
GCTATCTACC TGGCAGGGAA AGAG

24

SEQ ID NO:78  
SEQUENCE LENGTH: 25  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:78  
GAGTTTCITA CTATGATCTG GATTIC

25

SEQ ID NO:79  
SEQUENCE LENGTH: 25  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:79

GCAAAATGTA CTCAGCTTCA ATCAC	25
SEQ ID NO:80	
SEQUENCE LENGTH: 24	
SEQUENCE TYPE: nucleic acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: other nucleic acid, synthetic DNA	
SEQUENCE DESCRIPTION: SEQ ID NO:80	
GTAAATGCAG TACTGTTCTG ATCC	24
SEQ ID NO:81	
SEQUENCE LENGTH: 26	
SEQUENCE TYPE: nucleic acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: other nucleic acid, synthetic DNA	
SEQUENCE DESCRIPTION: SEQ ID NO:81	
GAATGCTTCA TTCTCATTTGT TTAAGG	26
SEQ ID NO:82	
SEQUENCE LENGTH: 24	
SEQUENCE TYPE: nucleic acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: other nucleic acid, synthetic DNA	
SEQUENCE DESCRIPTION: SEQ ID NO:82	
GTCACTAGGA TTCCACAGAA CTTC	24
SEQ ID NO:83	
SEQUENCE LENGTH: 22	
SEQUENCE TYPE: nucleic acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: other nucleic acid, synthetic DNA	
SEQUENCE DESCRIPTION: SEQ ID NO:83	
GAGGTAGGGC TTCCCTTCGC TA	22
SEQ ID NO:84	
SEQUENCE LENGTH: 25	
SEQUENCE TYPE: nucleic acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: other nucleic acid, synthetic DNA	

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SEQUENCE DESCRIPTION: SEQ ID NO:84  
GCATAACAAG TGACAGGGTT AGTTA

25

SEQ ID NO:85  
SEQUENCE LENGTH: 22  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:85  
GGTGCTCCCT CCTTACACTG GT

22

SEQ ID NO:86  
SEQUENCE LENGTH: 23  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:86  
GACTACACAT AAACCCACCC CAG

23

SEQ ID NO:87  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:87  
GGGTACAGGA TTTCTAAGAA GTGG

24

SEQ ID NO:88  
SEQUENCE LENGTH: 25  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:88  
GGAGAAAATT TCAGCTCATC TGAAG

25

SEQ ID NO:89  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:89  
GCTGAAGTTA AGCATTATA CGCC 24

SEQ ID NO:90  
SEQUENCE LENGTH: 23  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:90  
GGGGCTGTAA TGTGCAATGA TGT 23

SEQ ID NO:91  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:91  
GACAGAACC TAATAACAGC TGTC 24

SEQ ID NO:92  
SEQUENCE LENGTH: 22  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:92  
GTCTTAGGCA CTTGTCACTA GG 22

SEQ ID NO:93  
SEQUENCE LENGTH: 22  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:93  
GAGGGGACTT CCAAGAGTCT CT 22

SEQ ID NO:94  
SEQUENCE LENGTH: 25  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:94  
GTCTTCAGGA AAATTGTA GT TACAG 25

SEQ ID NO:95  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:95  
GTTACAAACA CACACCGAAGT TCCT 24

SEQ ID NO:96  
SEQUENCE LENGTH: 22  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:96  
GACTTCCTAA GGCACACTCA GC 22

SEQ ID NO:97  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:97  
GTTTAATAC ACCTCTCAGGTC ATGA 24

SEQ ID NO:98  
SEQUENCE LENGTH: 22  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:98  
GTCGCCAAGG CTGCTAGTGCA AT 22

SEQ ID NO:99  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid

Sequence Data from GenBank

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:99  
GAAATAGGTA TCCCTTGATG TCGA 24

SEQ ID NO:100  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:100  
GACCAAGAAC TCAAGTTCATC AGTT 24

SEQ ID NO:101  
SEQUENCE LENGTH: 22  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:101  
GAATGAACCA GACCCAGGAC AG 22

SEQ ID NO:102  
SEQUENCE LENGTH: 22  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:102  
GCCTTGTATG TATGCCCTGTG CC 22

SEQ ID NO:103  
SEQUENCE LENGTH: 21  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:103  
AAGAGTCCAC CAGGCCATGG A 21

SEQ ID NO:104  
SEQUENCE LENGTH: 23

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SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:104  
TACCTTGTTG ACTTCTAGCT GAG

23

SEQ ID NO:105  
SEQUENCE LENGTH: 17  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:105  
GTTTTTTTTT TTTTTTA

17

SEQ ID NO:106  
SEQUENCE LENGTH: 17  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:106  
GTTTTTTTTT TTTTTTG

17

SEQ ID NO:107  
SEQUENCE LENGTH: 17  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:107  
GTTTTTTTTT TTTTTTC

17

SEQ ID NO:108  
SEQUENCE LENGTH: 18  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:108  
CAGACTGATG GATATCAA

18

SEQ ID NO:109

SEQUENCE LENGTH: 22  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:109  
ATGAAAGTGC CAGTGTGCCA TG

22

SEQ ID NO:110  
SEQUENCE LENGTH: 22  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:110  
CCCATCACCA TCTTCCAGGA GC

22

SEQ ID NO:111  
SEQUENCE LENGTH: 26  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:111  
TTCACCACCT TCTTGATGTC ATCATA

26